

BBI-009C3CN2



SEQUENCE LISTING

<110> BUJARD, Hermann
GOSSEN, Manfred

<120> Transgenic Organisms Having Tetracycline-Regulated Transcriptional
Regulatory Systems (as amended)

<130> BBI-009C3CN2

<140> 09/874389

<141> 2001-06-04

<150> 09/161902

<151> 1998-09-28

<150> 08/487472

<151> 1995-06-07

<150> 08/383754

<151> 1995-02-03

<150> 08/275876

<151> 1994-07-15

<150> 08/270637

<151> 1994-07-01

<150> 08/250452

<151> 1994-06-14

<150> 08/076327

<151> 1993-06-14

<150> 08/076726

<151> 1993-06-14

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1008

<212> DNA

<213> Artificial Sequence

<220>

<223> Tet activator fusion

<220>

<221> exon

<222> (1)...(1008)

<220>

<221> mRNA

<222> (1)...(1008)

<220>

<221> misc_binding

<222> (1)...(207)

<220>

<221> misc_binding

<222> (208)...(335)

<220>

<221> CDS

<222> (1)...(1005)

<400> 1

| | |
|---|-----|
| atg tct aga tta gat aaa act aaa gtg att aac agc gca tta gag ctg | 48 |
| Met Ser Arg Leu Asp Lys Thr Lys Val Ile Asn Ser Ala Leu Glu Leu | |
| 1 5 10 15 | |
| ctt aat gag gtc gga atc gaa ggt tta aca acc cgt aaa ctc gcc cag | 96 |
| Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln | |
| 20 25 30 | |
| aag cta ggt gta gag cag cct aca ctg tat tgg cat gta aaa aat aag | 144 |
| Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys | |
| 35 40 45 | |
| cgg gct ttg ctc gac gcc tta gcc att gag atg tta gat agg cac cat | 192 |
| Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His | |
| 50 55 60 | |
| act cac ttt tgc cct tta aaa ggg gaa agc tgg caa gat ttt tta cgc | 240 |
| Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg | |
| 65 70 75 80 | |
| aat aag gct aaa agt ttt aga tgt gct tta cta act cat cgc aat gga | 288 |
| Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Thr His Arg Asn Gly | |
| 85 90 95 | |
| gca aaa gta cat tca gat aca cgg cct aca gaa aaa cag tat gaa act | 336 |
| Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr | |
| 100 105 110 | |
| ctc gaa aat caa tta gcc ttt tta tgc caa caa ggt ttt tca cta gag | 384 |
| Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu | |
| 115 120 125 | |
| aat gca tta tat gca ctc agc gct gtg ggg cat ttt act tta ggt tgc | 432 |
| Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys | |
| 130 135 140 | |
| gta ttg gaa gat caa gag cat caa gtc gct aaa gaa gaa agg gaa aca | 480 |
| Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr | |
| 145 150 155 160 | |
| cct act act gat agt atg ccg cca tta tta cga caa gct atc gaa tta | 528 |
| Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu | |
| 165 170 175 | |
| ttt gat cac caa ggt gca gag cca gcc ttc tta ttc ggc ctt gaa ttg | 576 |
| Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu | |
| 180 185 190 | |

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```

atc ata tgc gga tta gaa aaa caa ctt aaa tgt gaa agt ggg tcc gcg 624
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
      195                      200                      205

tac agc cgc gcg cgt acg aaa aac aat tac ggg tct acc atc gag ggc 672
Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
      210                      215                      220

ctg ctc gat ctc ccg gac gac gac gcc ccc gaa gag gcg ggg ctg gcg 720
Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
      225                      230                      235                      240

gct ccg cgc ctg tcc ttt ctc ccc gcg gga cac acg cgc aga ctg tcg 768
Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
      245                      250                      255

acg gcc ccc ccg acc gat gtc agc ctg ggg gac gag ctc cac tta gac 816
Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
      260                      265                      270

ggc gag gac gtg gcg atg gcg cat gcc gac gcg cta gac gat ttc gat 864
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
      275                      280                      285

ctg gac atg ttg ggg gac ggg gat tcc ccg ggt ccg gga ttt acc ccc 912
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
      290                      295                      300

cac gac tcc gcc ccc tac ggc gct ctg gat atg gcc gac ttc gag ttt 960
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
      305                      310                      315                      320

gag cag atg ttt acc gat ccc ctt gga att gac gag tac ggt ggg 1005
Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
      325                      330                      335

tag 1008

<210> 2
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> mutated Tn-10 derived Tet repressor

<400> 2
Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1      5      10      15
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
 20      25
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
 35      40      45
Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
 50      55      60
Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
 65      70      75      80
Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
 85      90      95
Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
 100     105     110

```

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
115 120 125
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
130 135 140
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145 150 155 160
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
165 170 175
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
180 185 190
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
195 200 205
Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
210 215 220
Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
225 230 235 240
Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
245 250 255
Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
260 265 270
Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
275 280 285
Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
290 295 300
His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
305 310 315 320
Glu Gly Met Phe Thr Asp Pro Leu Gly His Asp Glu Tyr Gly Gly
325 330 335

<210> 3
<211> 33
<212> DNA
<213> Herpes simplex virus

<220>
<221> CDS
<222> (1)...(33)

<400> 3
gac gcg cta gac gat ttc gat ctg gac atg ttg

33

<210> 4
<211> 11
<212> PRT
<213> Herpes simplex virus

<400> 4
Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
1 5 10

<210> 5
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> nuclear localization signal

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<400> 5

Met Pro Lys Arg Pro Arg Pro
1 5

<210> 6

<211> 569

<212> DNA

<213> Artificial Sequence

<220>

<223> Bidirectional promoter

<400> 6

```
gaattcgggg cgcgcggaggc tggatcgggc cccgtgtctt ctatggaggt caaacacagcg 60
tggatggcgt ctccaggcga tctgacgggt cactaaacga gctctgctta tataggctga 120
gtttaccact ccctatcagt gatagagaaa agtgaaagtc gagtttacca ctccctatca 180
gtgatagaga aaagtgaag tgcagtttac cactccctat cagtgataga gaaaagtga 240
agtcgagttt accactccct accagtgata gagaaaagtg aaagtcgagt ttaccactcc 300
ctatcagtga tagagaaaag tgaaagtcga gtttaccact ccctatcagt gatagagaaa 360
agtgaagtc gagtttacca ctccctatca gtgatagaga aaagtgaag tgcagctcg 420
taccgggtc gagtagcgt gtacgggtgg aggcctatat aagcagagct cgtttagtga 480
accgtcagat cgcctggaga cgccatccac gctgttttga cctccataga agacaccggg 540
accgatccag cctccgcggc cccgaattc 569
```

<210> 7

<211> 520

<212> DNA

<213> Artificial Sequence

<220>

<223> Bidirectional promoter

<400> 7

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agatctgcag ggtcgcctcg tgttcgaggc cacacgcgtc accttaatat gcgaagtgga 60
ccgatctcg agtttaccac tccctatcag tgatagagaa aagtgaagtc cgagtttacc 120
actccctatc agtgatagag aaaagtgaag gtcgagttta ccactcccta tcagtgatag 180
agaaaagtga aagtcgagtt taccactccc tatcagtgat agagaaaagt gaaagtcgag 240
tttaccactc cctatcagtg atagagaaaa gtgaaagtcg agtttaccac tccctatcag 300
tgatagagaa aagtgaagtc cgagtttacc actccctatc agtgatagag aaaagtgaag 360
gtcagagctc gtacccgggt cgagtaggcg tgtacgggtg gaggcctata taagcagagc 420
tcgtttagtg aaccgtcaga tcgcctggag acgcatcca cgctgttttg acctccatag 480
aagacaccgg gaccgatcca gcctccgcgg cccgaattc 520
```

<210> 8

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<221> mRNA

<222> (382)...(450)

<220>

<223> Tetracycline-responsive PhCMV-1 promoter

<400> 8

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gaattcctcg agtttaccac tccctatcag tgatagagaa aagtgaagtc cgagtttacc 60
actccctatc agtgatagag aaaagtgaag gtcgagttta ccactcccta tcagtgatag 120
agaaaagtga aagtcgagtt taccactccc tatcagtgat agagaaaagt gaaagtcgag 180
tttaccactc cctatcagtg atagagaaaa gtgaaagtcg agtttaccac tccctatcag 240
```

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```

tgatagagaa aagtgaaagt cgagtttacc actccctatc agtgatagag aaaagtgaaa 300
gtcgaagctcg gtacccgggt cgagtaggcg tgtacgggtg gaggcctata taagcagagc 360
tcgttttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 420
aagacaccgg gaccgatcca gcctccgcgg 450

```

```

<210> 9
<211> 450
<212> DNA
<213> Artificial Sequence

```

```

<220>
<221> mRNA
<222> (382)...(450)

```

```

<220>
<223> Tet-regulated promoter

```

```

<400> 9
gaattcctcg acccggttac cgagctcgac ttctactttt ctctatcact gatagggagt 60
ggtaaaactcg actttcactt ttctctatca ctgataggga gtggtaaact cgactttcac 120
ttttctctat cactgatagg gagtggtaaa ctgcactttc acttttctct atcactgata 180
gggagtggtta aactcgactt tcacttttct ctatcactga tagggagtgg taaactcgac 240
tttcaactttt ctctatcact gatagggagt ggtaaactcg actttcactt ttctctatca 300
ctgataggga gtggtaaact cgagtaggcg tgtacgggtg gaggcctata taagcagagc 360
tcgttttagtg aaccgtcaga tcgcctggag acgccatcca cgctgttttg acctccatag 420
aagacaccgg gaccgatcca gcctccgcgg 450

```

```

<210> 10
<211> 398
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Herpes simplex virus minimal tk promoter linked to
      ten tet operator sequences

```

```

<400> 10
gagctcgact ttcaactttt tctatcactg atagggagtg gtaaaactga ctttcaacttt 60
tctctatcac tgataggagg tggtaaactc gactttcact tttctctatc actgataggg 120
agtggtaaac tcgactttca cttttctcta tcaactgatg ggagtggtaa actcgacttt 180
cacttttctc tatcactgat agggagtggg aaactcgact ttcaactttt tctatcactg 240
atagggagtg gtaaaactga ctttcaacttt tctctatcac tgataggagg tggtaaactc 300
gagatccggc gaattcgaac acgcagatgc agtcggggcg gcgcgggtccg aggtccactt 360
cgcatattaa ggtgacgcgt gtggcctcga acaccgag 398

```

```

<210> 11
<211> 38
<212> DNA
<213> Escherichia coli

```

```

<220>
<221> misc_feature
<222> (1)...(38)
<223> class A tet operator

```

```

<400> 11
actttatcac tgataaaca acttatcagt gataaaga 38

```

```

<210> 12
<211> 38
<212> DNA

```

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<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(38)

<223> class B tet operator

<400> 12

actctatcat tgatagagtt ccctatcagt gatagaga

38

<210> 13

<211> 38

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(38)

<223> class C tet operator

<400> 13

agcttatcat cgataagcta gtttatcaca gttaaatt

38

<210> 14

<211> 38

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(38)

<223> class D tet operator

<400> 14

actctatcat tgatagggaa ctctatcaat gatagggga

38

<210> 15

<211> 38

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(38)

<223> Class E tet operator

<400> 15

aatctatcac tgatagagta ccctatcatc gatagaga

38

<210> 16

<211> 621

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(621)

<223> Tet repressor

<220>

<221> CDS

<222> (1)...(621)

<400> 16

| | |
|---|-----|
| atg tct aga tta gat aaa act aaa gtg att aac agc gca tta gag ctg | 48 |
| Met Ser Arg Leu Asp Lys Thr Lys Val Ile Asn Ser Ala Leu Glu Leu | |
| 1 5 10 15 | |
| ctt aat gag gtc gga atc gaa ggt tta aca acc cgt aaa ctc gcc cag | 96 |
| Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln | |
| 20 25 30 | |
| aag cta ggt gta gag cag cct aca ttg tat tgg cat gta aaa aat aag | 144 |
| Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys | |
| 35 40 45 | |
| cgg gct ttg ctc gac gcc tta gcc att gag atg tta gat agg cac cat | 192 |
| Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His | |
| 50 55 60 | |
| act cac ttt tgc cct tta gaa ggg gaa agc tgg caa gat ttt tta cgt | 240 |
| Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg | |
| 65 70 75 80 | |
| aat aag gct aaa act ttt aga tgt gct tta cta agt cat cgc gat gga | 288 |
| Asn Lys Ala Lys Thr Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly | |
| 85 90 95 | |
| gca aaa gta cat tta ggt aca cgg cct aca gaa aaa cag tat gaa act | 336 |
| Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr | |
| 100 105 110 | |
| ctc gaa aat caa tta gcc ttt tta tgc caa caa ggt ttt tca cta gag | 384 |
| Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu | |
| 115 120 125 | |
| aat gca tta tat gca ctc agc gct gtg ggg cat ttt act tta ggt tgc | 432 |
| Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys | |
| 130 135 140 | |
| gta ttg gaa gat caa gag cat caa gtc gct aaa gaa gaa agg gaa aca | 480 |
| Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr | |
| 145 150 155 160 | |
| cct act act gat agt atg ccg cca tta tta cga caa gct atc gaa tta | 528 |
| Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu | |
| 165 170 175 | |
| ttt gat cac caa ggt gca gag cca gcc ttc tta ttc ggc ctt gaa ttg | 576 |
| Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu | |
| 180 185 190 | |
| atc ata tgc gga tta gaa aaa caa ctt aaa tgt gaa agt ggg tcc | 621 |
| Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser | |
| 195 200 205 | |

<210> 17

<211> 207

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<212> PRT

<213> Escherichia coli

<400> 17

```

Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1          5          10          15
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
          20          25          30
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
          35          40          45
Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
          50          55          60
Thr His Phe Cys Pro Leu Glu Gly Glu Ser Trp Gln Asp Phe Leu Arg
65          70          75          80
Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asp Gly
          85          90          95
Ala Lys Val His Leu Gly Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
          100          105          110
Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
          115          120          125
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
          130          135          140
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
145          150          155          160
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Ala His Glu Glu Leu
          165          170          175
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
          180          185          190
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
          195          200          205

```

<210> 18

<211> 621

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (0)...(0)

<223> Mutated Tet repressor

<220>

<221> CDS

<222> (1)...(621)

<400> 18

```

atg tct aga tta gat aaa agt aaa gtg att aac agc gca tta gag ctg      48
Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1          5          10          15

ctt aat gag gtc gga atc gaa ggt tta aca acc cgt aaa ctc gcc cag      96
Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
          20          25          30

aag cta ggt gta gag cag cct aca ctg tat tgg cat gta aaa aat aag      144
Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
          35          40          45

cgg gct ttg ctc gac gcc tta gcc att gag atg tta gat agg cac cat      192

```

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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Ala | Leu | Leu | Asp | Ala | Leu | Ala | Ile | Glu | Met | Leu | Asp | Arg | His | His | | |
| 50 | | | | | | 55 | | | | | 60 | | | | | | |
| act | cac | ttt | tgc | cct | tta | aaa | ggg | gaa | agc | tgg | caa | gat | ttt | tta | cgc | 240 | |
| Thr | His | Phe | Cys | Pro | Leu | Lys | Gly | Glu | Ser | Trp | Gln | Asp | Phe | Leu | Arg | | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | | |
| aat | aag | gct | aaa | agt | ttt | aga | tgt | gct | tta | cta | agt | cat | cgc | aat | gga | 288 | |
| Asn | Lys | Ala | Lys | Ser | Phe | Arg | Cys | Ala | Leu | Leu | Ser | His | Arg | Asn | Gly | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| gca | aaa | gta | cat | tca | gat | aca | cgg | cct | aca | gaa | aaa | cag | tat | gaa | act | 336 | |
| Ala | Lys | Val | His | Ser | Asp | Thr | Arg | Pro | Thr | Glu | Lys | Gln | Tyr | Glu | Thr | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| ctc | gaa | aat | caa | tta | gcc | ttt | tta | tgc | caa | caa | ggg | ttt | tca | cta | gag | 384 | |
| Leu | Glu | Asn | Gln | Leu | Ala | Phe | Leu | Cys | Gln | Gln | Gly | Phe | Ser | Leu | Glu | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| aat | gca | tta | tat | gca | ctc | agc | gct | gtg | ggg | cat | ttt | act | tta | ggg | tgc | 432 | |
| Asn | Ala | Leu | Tyr | Ala | Leu | Ser | Ala | Val | Gly | His | Phe | Thr | Leu | Gly | Cys | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| gta | ttg | gaa | gat | caa | gag | cat | caa | gtc | gct | aaa | gaa | gaa | agg | gaa | aca | 480 | |
| Val | Leu | Glu | Asp | Gln | Glu | His | Gln | Val | Ala | Lys | Glu | Glu | Arg | Glu | Thr | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| cct | act | act | gat | agt | atg | ccg | cca | tta | tta | cga | caa | gct | atc | gaa | tta | 528 | |
| Pro | Thr | Thr | Asp | Ser | Met | Pro | Pro | Leu | Leu | Arg | Gln | Ala | Ile | Glu | Leu | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| ttt | gat | cac | caa | ggg | gca | gag | cca | gcc | ttc | tta | ttc | ggc | ctt | gaa | ttg | 576 | |
| Phe | Asp | His | Gln | Gly | Ala | Glu | Pro | Ala | Phe | Leu | Phe | Gly | Leu | Glu | Leu | | |
| | | 180 | | | | | | 185 | | | | | 190 | | | | |
| atc | ata | tgc | gga | tta | gaa | aaa | caa | ctt | aaa | tgt | gaa | agt | ggg | tcc | | 621 | |
| Ile | Ile | Cys | Gly | Leu | Glu | Lys | Gln | Leu | Lys | Cys | Glu | Ser | Gly | Ser | | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |

<210> 19
 <211> 207
 <212> PRT
 <213> Escherichia coli

<400> 19
 Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
 1 5 10 15
 Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
 20 25 30
 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
 35 40 45
 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
 50 55 60
 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
 65 70 75 80
 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
 85 90 95
 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
 100 105 110

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```

Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
      115              120              125
Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
      130              135              140
Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
      145              150              155              160
Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
      165              170              175
Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
      180              185              190
Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser
      195              200              205

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<210> 20
<211> 192
<212> DNA
<213> Drosophila melanogaster

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<220>
<221> misc_feature
<222> (0)...(0)
<223> C64KR region

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<220>
<221> CDS
<222> (1)...(192)

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<400> 20
gac atg gaa aea gcg aca ccg gag acg atg gtc cat tgg att tgt ctg      48
Asp Met Glu Lys Ala Thr Pro Glu Thr Met Val His Trp Ile Cys Leu
  1              5              10              15

aag atg gag cca gct ctg tgg atg gcc att aca gca aca tcg cac ggc      96
Lys Met Glu Pro Ala Leu Trp Met Ala Ile Thr Ala Thr Ser His Gly
              20              25              30

gca agg cac agg aca ttc gtc ggg ttt tcc ggc tgc ctc cac cgc aaa      144
Ala Arg His Arg Thr Phe Val Gly Phe Ser Gly Cys Leu His Arg Lys
              35              40              45

tcc ctc acg tac cca gtg ata tgc ctg agc aaa ccg agc cag agg att      192
Ser Leu Thr Tyr Pro Val Ile Cys Leu Ser Lys Pro Ser Gln Arg Ile
  50              55              60

```

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<210> 21
<211> 64
<212> PRT
<213> Drosophila melanogaster

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<400> 21
Asp Met Glu Lys Ala Thr Pro Glu Thr Met Val His Trp Ile Cys Leu
  1              5              10              15
Lys Met Glu Pro Ala Leu Trp Met Ala Ile Thr Ala Thr Ser His Gly
              20              25              30
Ala Arg His Arg Thr Phe Val Gly Phe Ser Gly Cys Leu His Arg Lys
              35              40              45
Ser Leu Thr Tyr Pro Val Ile Cys Leu Ser Lys Pro Ser Gln Arg Ile
  50              55              60

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<210> 22
 <211> 816
 <212> DNA
 <213> Avian erythroblastosis virus

<220>
 <221> misc_feature
 <222> (1)...(816)
 <223> v-erbA oncogene

<220>
 <221> CDS
 <222> (1)...(816)

<221> misc_feature
 <222> (0)...(0)
 <223> v-erbA oncogene

<400> 22
 ctg gac gac tcg aag cgc gta gcc aag cgg aag ctg atc gag gag aac 48
 Leu Asp Asp Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Glu Asn
 1 5 10 15

cgg gag cgg cga cgc aag gag gag atg atc aaa tcc ctg cag cac cgg 96
 Arg Glu Arg Arg Arg Lys Glu Glu Met Ile Lys Ser Leu Gln His Arg
 20 25 30

ccc agc ccc agc gca gag gag tgg gag ctg atc cac gtg gtg acc gag 144
 Pro Ser Pro Ser Ala Glu Glu Trp Glu Leu Ile His Val Val Thr Glu
 35 40 45

gcg cac cgc agc acc aac gcg cag ggc agc cac tgg aag cag agg agg 192
 Ala His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg
 50 55 60

aaa ttc ctg ctc gaa gat atc ggt cag tgc ccc atg gcc tcc atg ctt 240
 Lys Phe Leu Leu Glu Asp Ile Gly Gln Ser Pro Met Ala Ser Met Leu
 65 70 75 80

gac ggg gac aaa gtg gac ctg gag gcg ttc agc gag ttt aca aaa atc 288
 Asp Gly Asp Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile
 85 90 95

atc acg ccg gcc atc acc cgc gtg gtc gac ttt gcc aaa aac ctg ccc 336
 Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys Asn Leu Pro
 100 105 110

atg ttc tgc gag ctg ccg tgc gag gat cag atc atc ctg ctg aag ggc 384
 Met Phe Ser Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly
 115 120 125

tgc tgc atg gag atc atg tgc ctg cgc gcc gcc gtg cgc tac gac ccc 432
 Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro
 130 135 140

gag agc gaa acg ctg acg ctg agc ggg gaa atg gcc gtc aaa cgc gag 480
 Glu Ser Glu Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu
 145 150 155 160

cag ttg aag aac gga ggg ctg ggg gtc gtg tct gat gcc atc ttc gac 528
 Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Asp
 165 170 175

ctc ggc aag tcg ctg tct gcc ttc aac ctg gac gac acc gag gtg gcc 576
 Leu Gly Lys Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala
 180 185 190

ctg ctg cag gcc gtg ctg ctc atg tcc tca gac cgg acg ggg ctg atc 624
 Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Thr Gly Leu Ile
 195 200 205

tgc gtg gat aag ata gag aag tgc cag gag tcg tag ctg ctg gcg ttc 672
 Cys Val Asp Lys Ile Glu Lys Cys Gln Glu Ser * Leu Leu Ala Phe
 210 215 220

gag cac tac atc aac tac cgc aaa cac aac att ccc cac ttc tgg tcc 720
 Glu His Tyr Ile Asn Tyr Arg Lys His Asn Ile Pro His Phe Trp Ser
 225 230 235

aag ctg ctg atg aag gtg gcg gac ctg cgc atg atc ggc gcc tac cac 768
 Lys Leu Leu Met Lys Val Ala Asp Leu Arg Met Ile Gly Ala Tyr His
 240 245 250 255

gcc agc cgc ttc ctg cac atg aag gtg gag tgc ccc acc gag ctc tcc 816
 Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Ser
 260 265 270

<210> 23

<211> 272

<212> PRT

<213> Avian erythroblastosis virus

<400> 23

Leu Asp Asp Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Glu Asn
 1 5 10 15
 Arg Glu Arg Arg Lys Glu Glu Met Ile Lys Ser Leu Gln His Arg
 20 25 30
 Pro Ser Pro Ser Ala Glu Glu Trp Glu Leu Ile His Val Val Thr Glu
 35 40 45
 Ala His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg
 50 55 60
 Lys Phe Leu Leu Glu Asp Ile Gly Gln Ser Pro Met Ala Ser Met Leu
 65 70 75 80
 Asp Gly Asp Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile
 85 90 95
 Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys Asn Leu Pro
 100 105 110
 Met Phe Ser Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly
 115 120 125
 Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro
 130 135 140
 Glu Ser Glu Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu
 145 150 155 160
 Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Asp
 165 170 175
 Leu Gly Lys Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala
 180 185 190
 Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Thr Gly Leu Ile
 195 200 205
 Cys Val Asp Lys Ile Glu Lys Cys Gln Glu Ser Tyr Leu Leu Ala Phe

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| | | | | |
|---|-----|-----|-----|-----|
| 210 | | 215 | | 220 |
| Glu His Tyr Ile Asn Tyr Arg Lys His Asn Ile Pro His Phe Trp Ser | | | | |
| 225 | | 230 | | 240 |
| Lys Leu Leu Met Lys Val Ala Asp Leu Arg Met Ile Gly Ala Tyr His | | | | |
| | 245 | | 250 | 255 |
| Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Ser | | | | |
| | 260 | | 265 | 270 |

<210> 24
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polylinker

<400> 24
 tccccgggta actaagtaag gatcc 25

<210> 25
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polylinker

<400> 25
 agtgggtccc cgggtgacat ggaa 24

<210> 26
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Polylinker

<400> 26
 Ser Gly Ser Pro Gly Asp Met Glu
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<210> 27
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Polylinker

<400> 27
 agtgggtccc cgggtctgga cgac 24

<210> 28
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

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<223> Polylinker

<400> 28

Ser Gly Ser Pro Gly Leu Asp Asp
1 5